

FIGURE 1

CTCTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTG
AGAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGAC
CC
><MET {trans=1-s, dir=f, res=1}
ATGCTGCATCCAGAGACCTCCCTGGCCGGGGCATCTCCTGGCTGTGCTCCTGGCCCTC
CTTGGCACCACCTGGCAGAGGTGTGGCACCCAGCTGCAGGAGCAGGCTCCGATGGCC
GGAGCCCTGAACAGGAAGGAGAGTTCTTGCTCCTCCCTGCACAACCGCCTGCGCAGC
TGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAA
CTGGCTCAAGCCAGGGCAGCCCTGTGGAATCCAAACCCGAGCCTGGCATCCGGCCTG
TGGCGCACCTGCAAGTGGCTGGAACATGCAGCTGCTGCCCGCGGGCTTGGCGTCCTT
GTTGAAGTGGTCAGCTATGGTTGCAGAGGGCAGCGGTACAGCCACGCCAGGAGAG
TGTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTGCTGGGCCACCTCAAGCCAG
CTGGGCTGTGGCGGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAACGCTTTGTCTGT
GCCTACTCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAACG
GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTCAAAGCCTGGGACCAT
GCAGGGGGCTCTGTGAGGTCCCCAGGAATCCTGTGCACTGAGCTGCCAGAACCATGGA
CGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGAGATACTGC
CAAGTGAGGTGCAGCCTGCAGTGTGCACGGCCGGTCCGGGAGGAGGTGCTCGTGC
GTCTGTGACATCGGCTACGGGGAGCCCAGTGTGCCACCAAGGTGCATTTCCCTCCAC
ACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTCAGAGGCAGACACCTAT
TACAGAGCCAGGATGAAATGTCAGAGGAAAGGCCGGGTGCTGGCCAGATCAAGAGCCAG
AAAGTGCAGGACATCCTGCCCTCTATCTGGGCCCTGGAGACCACCAACGAGGTGACT
GACAGTGACTTCGAGACCAGGAACCTCTGGATCGGGCTCACCTACAAGACGCCAAGGAC
TCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCCTCACAGTTGCTTTGGCAGCCT
GACAACCACGGCTGGTGTGGCTGAGTGCTGCCATGGGTTTGGCAACTGCGTGGAGCTG
CAGGCTTCAGCTGCCCTCACTGGAACGACCGCCTGCAAAACCGAAACCGTTACATC
TGCCAGTTGCCCTAGGAGCACATCTCCGGTGGGGCCAGGGCTCTGAGGCCTGACCACA
TGGCTCCCTCGCCTGCCCTGGGAGCACCAGGCCCTGCTTACCTGTCTGCCACCTGTCTGG
AACAAAGGCCAGGTTAAGACCACATGCCCTATGTCAAAGAGGTCTCAGACCTGCAAA
TGCCAGAAGTGGGCAGAGAGAGGGCAGGGAGGCCAGTGAGGGCCAGGGAGTGAGTGTAG
AAGAAGCTGGGCCCTCGCCTGCTTTGATTGGAAAGATGGCCTCAATTAGATGGCGA
AGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTTCCACCTGGCCAGACCTG
TGGGGCAGCGGAGCTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAGCT
GAAAAA

FIGURE 2

1 CTCTTTGTC CACCAAGCCCA GCCTGACTCC TGGAGATTGT GAATAGCTCC ATCCAGCCTG AGAAACAAGC CGGGTGGCTG AGCCAGGCTG TGCACGGAGC
 GAGAAAACAG GTGGTGGGGT CGGACTGAGG ACCTCTAACCA CTTATCGAGG TAGGTGGAC TCTTGTTCG GCCCAGCGAC TCGGTCCGAC ACGTGCTCG
 101 ACCTGACGGG CCCAACAGAC CCATGCTGCA TCCAGAGACC TCCCCCTGGCC GGGGGCATCT CCTGGCTGTG CTCTGGCCC TCCTTGGCAC CACCTGGCA
 TGGACTGCC GGGTTGTCTG GGTACGACGT AGGTCTCTGG AGGGGACCGG CCCCCGTTAGA GGACCGACAC GAGGACCGGG AGGAACCGTG GTGGACCCGT
 1 M L H P E T S P G R G H L L A V L L A L L G T T W A
 *MET
 201 GAGGTGTGGC CACCCAGCT GCAGGAGCAG GCTCCGATGG CGGGAGCCCT GAACAGGAAG GAGAGTTCT TGCTCTCTC CCTGCACAAC CGCCTGGCA
 CTCCACACCG GTGGGTCGA CGTCTCTGTC CGAGGCTACC GGCTCGGGG CTITGCTCTC CTCTCAAGA ACAGGAGAG GGACGTGTTG GCGGACCGGT
 27 E V W P P Q L Q E Q A P M A G A L N R K E S F L L L S L H N R L R S
 301 GCTGGGTCGA GCCCCCTGCG GCTGACATGC GGAGGCTGGA CTGGAGTGAC AGCCTGGCCC AACTGGCTCA AGCCAGGCA GCCCCCTGTG GAATCCAAAC
 CGACCCAGGT CGGGGACGC CGACTGTACG CCTCCGACCT GACCTCACTG TCGGAACGGG TTGACCGAGT TCGGTCCCGT CGGGAGACAC CTTAGGGTTG
 61 W V Q P P A A D M R R L D W S D S L A Q L A Q A R A A L C G I P T
 401 CCCGAGCCTG GCATCGGCC TGTGGCGAC CCTGCAAGTC GGCTGGAACA TGCAAGCTGT GCCCCGGGGC TTGGCTCTT TTGTTGAAGT GGTCACCGTA
 GGGCTGGAC CGTAGGCCG ACACCGCGTGG GGACCTTGAC CCGACCTTGAC AGCTGACGA CGGGCGCCCG AACCGCAGGA AACAACTTCA CCAGTCGGAT
 94 P S L A S G L W R T L Q V G W N M Q L L P A G L A S F V E V V S L
 501 TGGTTTGACAG AGGGGAGCG GTACAGCCAC GCGGCAGGAG AGTGTGCTCG CAACGCCACC TGCAACCACT ACACCGAGCT CGTGTGGCC ACCTCAAGCC
 ACCAACCGTC TCCCCGTCGC CATGTGGTG CGCCGCTCTC TCACACGAGC GTTGGGTGG ACGTGGTGA TGTGCGTGA CCACACCCGG TGGAGTTGCG
 127 W F A E G Q R Y S H A A G E C A R N A T C T H Y T Q L V W A T S S Q
 601 AGCTGGCTG TGGGGGGCAC CTGTGCTCTG CAGGCCAGAC AGCGATAGAA GCCTTGTCT GTGCTACTC CCCCCGGAGC AACTGGGAGG TCAACGGGAA
 TCGACCCGAC ACCCGCCGTG GACACGAGAC GTCCGGCTCTG TCGCTATCTT CGAAACAGA CACGGATGAG GGGGCTCCG TTGACCCCTCC AGTTGCCCT
 161 L G C G R H L C S A G Q T A I E A F V C A Y S P G G N W E V N G K
 701 GACAATCATC CCCTATAAGA AGGGTGGCTG GTGTTGCTC TGCAACGCCA GTGCTCAGG CTGCTCTAAA GCGTGGGACC ATGCAGGGGG GCTCTGTGAG
 CTGTTAGTAG GGGATATTCT TCCCACGGAC CACAAGCAG ACGTGTGGT CACAGAGTCC GACGAAGTTT CGGACCTCTGG TACGTCCCCC CGAGACACTC
 194 T I I P Y K R G A W C S L C T A S V S G C F K A W D H A G G L C E
 801 GTCCCCAGGA ATCCTGTGCG CATGAGCTGC CAGAACCATG GACGCTCAA CATCACCAAC TGCCACTGCC ACTGTCCCCC TGGCTACAGC GCGAGATACT
 CAGGGCTCT TAGGAACAGC GTACTCGACG GTCTGGTAC CTGCAGAGTT GTAGTGTGG ACGGTACGG TGACAGGGGG ACCGATGTGC CGCTCTATGA
 227 V P R N P C R M S C Q N H G R L N I S T C H C H C P P G Y T G R Y C
 901 GCCAAGTGAG GTGCGGCCCTG CAGTGTGTC ACAGGGCGTT CGGGGAGGAG GAGTGCTCGT CGCTCTGTGA CATCGCTAC GGGGGAGCCC AGTGTGCCAC
 CGGTCTACTC CACGTGGAC GTCACACACG TGCCGCCAA GGCCCTCTC CTCACAGCA CGCAGACACT GTAGCGATG CCCCCCTGGG TCACACGGTG
 261 Q V R C S L Q C V H G R F R E E E C S C V C D I G Y G G A Q C A T
 1001 CAAGGTGCAT TTCCCTTCC ACACCTGTGA CCTGAGGATC GACGGAGACT GCTTCATGGT GTCTTCAGAG GCAGACACCT ATTACAGAC CAGGATGAAA
 GTTCCACGTA AAAGGAAGG TGTGACACT GGACTCTTAG CTGCCCTCTGA CGAAGTACCA CAGAAGTCTC CGTCTGTGA TAATGTCTCG GTCTACTTT
 294 K V H F P F H T C D L R I D G D C F M V S S E A D T Y Y R A R M K
 1101 TGTCAAGAGGA AAGGGGGGT GCTGGGGCAG ATCAAGAGCC AGAAAGTGCA GGACATCCTC GCGCTCTATC TGGGGCCCTT GGAGACCAC AACGAGGTGA
 ACAGTCTCCT TTCCGCCCA CGACGGGTC TAGTTCTCGG TCTTTCACGT CCTGTTAGAG CGGAAGATAG ACCCGGCGGA CCTCTGGTGG TTGCTCCACT
 327 C Q R K G G V L A Q I K S Q K V Q D I L A F Y L G R L E T T N E V T
 1201 CTGACAGTGA CTTGAGACCC AGGAACCTCT GGATGGGCT CACCTACAAG ACCGCAAGG ACTCTCTCCG CTGGGCCACA CGGGAGCACC AGGCCTTCAC
 GACTGTCACT GAAGCTCTGG TCCCTGAAAGA CCTAGCCGA GTGGATGTC TGCGGTTCC TGAGGAAGGC GACCCGGTGT CCCCCCTGG TCCGGAACTG
 361 D S D F E T R N F W I G L T Y K T A K D S F R W A T G E H Q A F T
 1301 CAGTTTGCC TTGGGCAGC CTGACAACCA CGGGCTGGTG TGGCTAGTG CTGCATGGG GTTGGCAAC TCGCTGGAGC TGCAGGCTTC AGCTGCCCTC
 GTCAAAACGG AAACCGCTCG GACTGTGGT GCGCGACAC ACCGACTCAC GACGGTACCC CAAACCGTIG ACACCCCTCG AGCTCCGAG TCGACGGAG
 394 S F A F G Q P D N H G L V W L S A A M G F G N C V E L Q A S A A F
 1401 AACTGGAAACG ACCAGCGCTG CAAACCCGA AACCGTACA TCTGCCAGTT TGCCAGGAG CACATCTCC GGTGGGGCCC AGGGTCTGA GGCCTGACCA
 TTGACCTTGC TGGTGGCAGC GTTTGGGT TTGGCAATGT AGACGGTCAA ACAGGCTCTC GTGTAGAGGG CCACCCGGG TCCCAAGGACT CGGGACTGGT
 427 N W N D Q R C K T R N R Y I C Q F A Q E H I S R W G P G S O
 1501 CATGGCTCCC TCGCTGCC TGGGAGCACC GGCTCTGCTT ACCTGTCTGC CCACCTGTCT CGAACAAAGGG CGAGGTTAAG ACCACATGCC TCATGTCCAA
 GTACCGAGGG AGCGGACGGG ACCCTCGTGG CCGAGACGAA TGGACAGACG GGTGGACAGA CCTTGTCTCC GGTCCAATTC TGGTGTACGG AGTACAGGTT
 1601 AGAGGTCTCA GACCTTGCAC AATGCCAGAA GTTGGGAGA GAGAGCAGG GAGGCCAGTG AGGGCCAGGG AGTGTAGTGT AGAAGAAGCT GGGGCCCTC
 TCTCCAGAGT CTGGAACGTC TTACCGCTCTT CAACCCGCTC CTCTCCGTCAC TCCCGGCTCC TCACTCACAA TCTCTCTGA CCCCCGGGAAAG
 1701 GCCTGCTTTT GATTGGGAAG ATGGGCTTCA ATTAGATGGC GAAGGAGAGG ACACCGCCAG TGGTCCAAAAGGCTGCTCT CTCCACCTG GCCCAGACCC
 CGGACGAAA CTAACCCCTTC TACCCGAAGT TAATCTACCG CTTCCTCTCC TGTGGCGTC ACCAGGTTTT TCCGACGAGA GAAGGTGGAC CGGGTCTGGG
 1801 TGTGGGCAG CGGAGCTTCC CTGTGGCATG AACCCACGG GGTATTAAT TATGAATCAG CTGAAAAAAA AAAAAA
 ACACCCCGTC GCCTCGAAGG GACACCGTAC TTGGGTTGCC CCATAATTAA ATACTTAGTC GACTTTTTTT TTTTTT

FIGURE 3

><homology to cysteine-rich secretory proteins>

><signal peptide>

MLHPETSPGRGHLLAVLLALLGTTWA

><start mature protein>

EVWPPQLQEQQAPMAGALNRKESFLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLA
QARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLSWFAEGQRYSHAA
GECAR

><potential N-glycosylation site>

NATCTHYTQLVWATSSQLGCGRHLCAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKK
GAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCMSCQNHGRL

><potential N-glycosylation site>

NISTCH

><EGF-like domain cysteine pattern signature>

CHCPCPGYTGRYCVRCQLQCVHGRFREEECS

><EGF-like domain cysteine pattern signature>

CVCDIGYGGAQCATKVHFPFHTCDLRIDGDCFMSSEADTYYRARMKCQRKGGVLA
QIKSQKVQDILAFYLGRLLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAF
TSFAFGQPDNHGLVWLSAAMFGGN

><C-type lectin domain signature (CVELQASAAFNWNDQRCKTRNRYIC)>

CVELQASAAFNWNDQRCKTRNRYICQFAQEHIRWGPGS

FIGURE 4

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</usr/seqdb2/sst/dNA/Dnaseqs.min/ss.DNA44176
<subunit 1 of 1, 455 aa, 1 stop
<MW: 50478, pI: 8.44, NX(S/T): 2
< 1 10 20 30 40 50 60 70
< | | | | | | | |
< MILHPETSEGRGHLLAVILLALLGTTWAEVWPPQIQQAPMAGALNTRKESFLILLSLHNRLRSWVQPPAADM
< 71 80 90 100 110 120 130 140
< | | | | | | | |
< RLDWSDSLQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWEAEGQRYSHAAGE
< 141 150 160 170 180 190 200 210
< | | | | | | | |
< CARNATCTHYTQLWATSSSQLGCGRHILCSAGQTAEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSSLCTAS
< 211 220 230 240 250 260 270 280
< | | | | | | | |
< VSGCFKAWDHAGGLCEVPRNPCRMSQCQNHGRLNISTCHCCHCPCPGYTGRYCQVRCSSLQCVHGRFREECSC
< 281 290 300 310 320 330 340 350
< | | | | | | | |
< VCDIGYGGQAQCATKVHFPEHTCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYL
< 351 360 370 380 390 400 410 420
< | | | | | | | |
< GRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHLVWLSAAMGFGNCVEL
< 421 430 440 450
< | | | | |
< QASAAFNWNDQRCKTRNRYICQFAQEHIISRWGPGS
```

FIGURE 5A

2989336	1	GCTGGGAAGANGGCCAGAAAGGCAGCTGGCAGCAGACTCCAGGGTCTGA
W79362	1	ACAG
.....	
<consen01>	1	ACAG
2989336	51	GTGGGCCAACCTGACTACNCGGCCCAGGGCTCACCTACAAGACCGCCA
W79362	5	TGACTTCGAGACCAGGAACCTCTGGATCGGGCTCACCTACAAGACCGCCA
.....
<consen01>	5	TGACTTCGAGACCAGGAACCTCTGGATCGGGCTCACCTACAAGACCGCCA
2989336	101	AGGACTCCTCCGCTGGGCCACAGGGGAGCACCAGGCCTCACCAAGTTTT
W79362	55	AGGACTCCTCCGCTGGGCCACAGGGGAGCACCAGGCCTCACCAAGTTTT
.....
<consen01>	55	AGGACTCCTCCGCTGGGCCACAGGGGAGCACCAGGCCTCACCAAGTTTT
2989336	151	GCCTTGCGCAGCCTGACAACCACGGGTTGGCAACTGCGTGGAGCTGCA
W79362	105	GCCTTGCGN-AGCCTGACAACCACGGGTTGGCAACTGCGTGGAGCTGCA
2554374	1	TGCGTGGAGCTGCA
.....
<consen01>	105	GCCTTGCGCAGCCTGACAACCACGGGTTGGCAACTGCGTGGAGCTGCA
2989336	201	GG-TTCAGCTGCCTCAACTGGAACAACCAGCG-TGCAAAACCCGAAACC
W79362	154	GGCTTCAGCTGCCTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACC
2554374	15	GGCTTCAGCTGCCTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACC
2992967	1	AACC
.....
<consen01>	155	GGCTTCAGCTGCCTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACC
2989336	249	GTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGNNCAG
W79362	204	GTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGCCATGG
2554374	65	GTTACATCTGCCAGTTGGTGAGGGACTCCTGAGGCTCCCTTC-TG
2992967	5	GTTACATCTGCCAGTCTGCCAGGNGCACATCTCCGGTGGGCCA-GG
2673172	1	GGCCA-GG
.....
<consen01>	205	GTTACATCTGCCAGTTGCCAGGAGCACATCTCCGGTGGGCCA GG
W79362	254	GTCCTGATGGCCTGACCACATGGCTCCCTGCCCTGGGAGCACCGG
2554374	114	ATCCCTG-ACCCTGGGGTGCTGCTGACCCGGTCCAGCCTGCAAGGGTAT
2992967	54	GTCCTGA-GGCCTGACCACATGGCTCCCTGCCCTGGGAGCACCGG
2673172	9	GTCCTGA-GGCCTGACCACATGGCTCCCTGCCCTGNGANCACCGG
.....
<consen01>	254	GTCCTGA GGCCTGACCACATGGCTCCCTGCCCTGGGAGCACCGG
W79362	304	CTCTGCTTACCTGTCTGCCACCTNGTCTGNAACAAGGGCCAAGGTTAAG
2554374	163	CTAGGTGGCAGGTTCAAGAGTGGGT-CTGGGCACACGGGCCA-TAGAGGA
2992967	103	CTCTGCTTACCTGTCTGCCACCT-GTCTGGAACAAGGGCCA-GGTAAAG
2673172	58	CTCTGCTTACCTGTCTGCCACCT-GTCTGGAACAAGGGCCA-GGTAAAG
.....
<consen01>	303	CTCTGCTTACCTGTCTGCCACCT GTCTGGAACAAGGGCCA GGTAAAG

FIGURE 5B

FIGURE 6

```
ACAGTGACTTCGAGACC
><39499.f1 {underline=1-24, dir=f}>
AGGAACCTCTGGATCGGGCTCACCTACAAGACC
><39499.p1 {underline=1-45, dir=f}>
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GGGCAGCCTGACAACCACGGGTTGGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTC
AACTGGAACGACCAGCGCTGCAAACCCGAAACCGTTACATCTGCCAGTTGCCAGGAG
CACATCTCCCAGGTGGGCCACGGGTCTGAGGCCTGACCACATGGCTCCCTGCCTGCC
TGGGAGCACCAGGTCTGCTTACCTGTCTGCCACCTGTCTGGAACAAGGGCCAGGTTAAG
ATCACATGCCCTCATGTCAAAGAGGTCTCAGACCTTGCACAAATGCCAGAAGTTGGCAGA
GAGAGGCAGGGAGGCCAGTGAGGGCGAGGGAGTGAGTGTAGAAGAAGCTGGGCCCTC
GCCTGCTTTGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGGGAGAGGACACCGCCAG
TGGTCCAAAAGGCTGCTCTTCCACCTGGCCAGACC
><39499.r1 {underline=1-24, dir=b}>
CTGTGGGGCAGCGGACTTCCCTGTGGCATGAACCCCACGGTAATTAAATTATGAATCAG
CTGAAAGAAGAAAAGTCGGCG
```

FIGURE 7

1 ACAGTGACTT CGGAGCCAGG AACTTCTGGAA TCGGGCTCAC CTACAAGACC GCCAAGGACTT CCTTCCGGCTG GGGCACAGGGG GAGGACCAAGG CCTTTCACCGA
TGTCACTGAA GCTCTGGTCC TGAAAGACCT AGCCCAGTGT GATGTTCTGG CGGTTCCTGA GGAAAGGGGAC CCGGGTCTCCC CTCGTTCTGCC GGAAGCTGGTC
^39499 .r1

101 TTTTGCCCTT GGGCAGCCTG ACAACCACGG GTTGGCAAC TGGCTGGAGC TGCAGGGCTTC AGCTCCCTTC AACCTGAAACG ACCAGGGCTG CAAACCCGA
AAACCGAAA CCCGTCGGAC TGTGGTGC CAAACCGTC ACACCGTTG ACCGACCTCG ACETCCCGAAG TCGACGGAAAG TTGACCTTGC TGGTGCAGC GTTTGGGT
^39499 .r1

201 AACCGTTACA TCTGCCAGTT TGGCCAGAG CACATCTCCC GTGGGGCCC AGGGTCTGA GGCCCTGACCA CATGGCCTCC TCGCCTGCC TGGGAGCCACC
TTGGCAATGT AGACGGTCAA AGGGGTCTTC GTGTAGAGG CCACCCGGG TCCCAGGACT CCGGACTGTT GTACCCGGG AGGGACGGG ACCCTCTGG
^39499 .r1

301 GGCTCTGCTT ACCTGTCTGC CACACTGTCT GGAAACAAGGG CCAGGTTAAG ATCACATGCC TCATGTCCAA AGAGGTCTCA GACCTTGAC AATGCCAGAA
CCGAGACGAA TGGACAGACG GTGGACAGA CCTTGTCTCC GGTCCAATTTC TAGTGTACGG AGTACAGGTT TCTCCAGAGT CTGGAACTG TTACGGTCTT
^39499 .r1

401 GTTGGCAGA GAGGGCAGG GAGGCCAGTG AGGGCAGGG AGTGAAGTGT AGAGAGGCTT GGGGCCCTTC GCCTGCTTTT GATTGGGAAG ATGGCCTCA
CAACCCGGCTCTCTCCGTC CTCGGTCAAC TCCGGTCCC TCACTCACAA TCTTCTTCGA CCCCAGGAAAG CGGACGAAAA CTAACCCCTC TACCCGAAGT
^39499 .r1

501 ATTAGATGGC GAAGGGAGGG ACACCCGCCAG TGGTCCAAA AGGGCTGCTCT CTTCCACCTG GCCCAGACCC TGTGGGGCAG CGGACTTCCC TGTGGCATGA
TAATCTACCG CTTCTCTCC TGTGGGGTCA ACCAGGTTTT TCCGACGAGA GAAGGTGGAC CGGGTCTGG ACACCCGTC GCCTGAAGGG ACACCGTACT
^39499 .r1

601 ACCCCACGGG TAATAAATT ATGAATCAGG TGAAAGAAGA AAAAGTGGC G
TGGGGTGGCC ATTAAATTAA TACTTAGTGTG ACTTTCTTCT TTTTCAAGCTG C

FIGURE 8

>1 S68683 cysteine-rich secretory protein 3 precursor - human (245 aa)
Score = 235 (82.7 bits), Expect = 5.2e-18, P = 5.2e-18
Identities = 51/157 (32%), Positives = 78/157 (49%), at 273,42, Frame = +3

DNA44176 273 LLSLHNRLRSWVQPPAADMRRLDWSDSLQAQARAALCGIPTPSLASGLWRTLQVGWNM
S68683 42 IVNKHNLRRAVSPPARNMILKMEWNKEAAANAQKWAQCNY-RHSNPKDRMTSLKCGENL
S68683 101 YMSSAS-SSWSQAIQSWSFDEVNDFDFGVGPKTPNAVVGHTQVVWYSSYLVGCGNAYCPN

DNA44176 453 QLLPAGLASFVEVVSILWFAEGORYSHAAGECARNATCTHYTQLVWATSSQLGGGRHLCSA
S68683 160 QKVVKYYYYVCQYCPAGNWA--NRLYVVPYEQGAPCASC

DNA44176 633 GQTAALEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC
S68683 160 QKVVKYYYYVCQYCPAGNWA--NRLYVVPYEQGAPCASC

FIGURE 9

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>8 ECCRISP3_1 cysteine-rich secretory protein-3 - Equus caballus (245 aa)
Score = 216 (76.0 bits), Expect = 5.8e-16, P = 5.8e-16
Identities = 71/242 (29%), Positives = 109/242 (45%), at 159,3, Frame = +3

```

DNA44176	159	LLAVLLALLGGTTAWEVWPPOLQEQQAPMAGALNRKE-SFLLLSLHNRLRSWVQPPAADMRR	
ECCRISP3_1	3	LLPVLL-FLAAVLLPFFPASQDDGFAALSITKSEVQKEIVNKHNDLRRTVSPLASNMLK	
DNA44176	336	LDWSDSLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVSLWFAEG	
ECCRISP3_1	62	MQWDSKTTATNAQNWANKCQLQHSAKAEDRAVGTMKCGENL-FMSSIPNSWSDAIQNWHDEV	
DNA44176	516	QRYSHAAGECARNATCATHYTOLVWATSSQLGGRHLCSAGQATAIEAFVCAYSPGGNWEVN	
ECCRISP3_1	121	HDFKYGVGPKTPNAVYGHYTQVWYSSYRGCGIAYCPKQGTLKYYVCQYCPAGNY-VN	
DNA44176	696	GKTIIPIYKKGAWCS-----LCTAS-----VSGCFCKAWDHAGGLCEVPRNPCRMS	
ECCRISP3_1	180	-KINTPYEQGTPCARCPGNCNDGLCTNSCEYEDLVSNCNDLSKKIAGCEHELLKNCKTTC	
DNA44176	831	QNHGRL	
ECCRISP3_1	239	QCENKI	

FIGURE 10